OIPE

RAW SEQUENCE LISTING DATE: 05/03/2002
PATENT APPLICATION: US/10/051,409 TIME: 16:14:23

Input Set : A:\12005-003001.TXT
Output Set: N:\CRF3\05032002\J051409.raw

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 4 <110> APPLICANT: Yang, Chu-Wen
 5         Tsou, Ann-Ping
 6         Chi, Chin-Wen
 7         Fann, Ming-Ji
 8         Chou, Chen-Kung
10 <120> TITLE OF INVENTION: CELL CYCLE REGULATOR PROTEIN
13 <130> FILE REFERENCE: 12005-003001
15 <140> CURRENT APPLICATION NUMBER: 10/051,409
16 <141> CURRENT FILING DATE: 2002-01-18
18 <150> PRIOR APPLICATION NUMBER: 60/262,885
19 <151> PRIOR FILING DATE: 2001-01-19
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23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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26 <211> LENGTH: 2424
27 <212> TYPE: DNA
28 <213> ORGANISM: Mus musculus
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33 cgaaacagac acttcggttt gaaggacgtc aacattccac tggaagggcg agagcttggt    180
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35 gtaaaaatgg tcctgagtga ccaacggaag cagctcctcc agaagtataa ggaagaaaaa    300
36 caacttcaaa aactgaaaga acagcgagag aaagccaaac gtggagtgtt caaagtgggt    360
37 ctctatagac ccgctgcgcc tggctttctt gtcacagacc agaggggtgc gaaagctgag    420
38 ccagaaaagg cttttccaca tactggacgg attacaagat caaagaccaa agaatatatg    480
39 gagcagacta agattggtag caggaatgtt cctaaagcaa cccagagtga ccaaagacaa    540
40 acttctgaaa aacaaccatt agacagagag agaaaagtta tgcagcctgt gctgttcacg    600
41 tcagggaaag ggactgaatc agcggctact cagagagcca agctgatggc ccgaacagtg    660
42 tcatccacta caagaaagcc agtcacaaga gccacgaatg agaaaggatc agaaagaatg    720
43 agaccaagtg gagggagacc tgccaaaaaa ccagaaggca agccggacaa ggtcattcct    780
44 tccaaagttg agcgggacga aaagcatttg gattcgcaga ccagggaaac aagtgaaatg    840
45 ggtctgctcg gagtcttccg agaagtggaa agcttgcctg caacagcccc tgcccaaggg    900
46 aaggaaagga gtcctttgc ccccaagcac tgtgtcttcc agcccccgtg tggtctgaag    960
47 agctaccagg tggctcccct gagccctaga agtgccaacg ctttcctgac acccaattgt   1020
48 gattggaacc agttaagacc agaagttttt agcactacaa ctcaagacaa agcaaatgaa   1080
49 atcttggtac agcaaggatt ggagtcgcta acagaccgta gtaaagaaca tgtcttaaat   1140
50 cagaagggcg cttctacttc agattcaaat cacgcttctg tgaaaggagt cccatgctct   1200
51 gaagggagcg aaggccagac ctctcagccc ccccacgatg tgccatactt cagaaaaatc   1260
52 ctccaatcag aaactgacag gctgacctcg cactgcctgg agtgggaggg aagctggac   1320
53 ctggacatct ctgatgaagc taaaggtctt atccgtacaa cggttggtca aacaagactc   1380
54 cttatcaagg agagattcag acagtttgaa ggactggtgg acaactgcga gtataaacgg   1440
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57 gacagcaata atccaagcaa aaaagtcctc cggaaaaaaa ttgtgcctgg tagaacaagc   1620
58 aaagcaaagc aggatgacga cggacgagcg gcagctagga gtcgccttgc tgccataaag   1680
59 aatgcaatga aaggcaggcc acagcaggaa gtgcaggccc acgcagcagc tccggagacc   1740
60 acaaaggaag ttgacaaaat agtgtttgac gctgggtttt tcagaatcga gagcccagtg   1800
61 aagtcattct cagtcctgtc ttctgaacgt cgttctcaaa gatttggaac acctctgtct   1860
62 gccagcaaag ttgtgcctga gggcagggct gcaggggacc ttctgagaca gaagatgcca   1920
63 ctgaagaagc cggaccctca gagcagcaag agtgagcatg ttgatcggac gttttcagat   1980
64 ggtcttgaaa gcaggtgcca cgtagaagac accccctgtc ctggagagca agattcaagt   2040
65 gacatagagc atgatgtaaa taaaataaat gtcaagatgg attgtttctc tgttgaaacg   2100
66 aatttgcctc ttcctgctgg tgatgctaat accaatcaaa aagaagcaat ctcagccgtg   2160
67 gaaggagcga gcactgcagt cacctcccag gatttgctga tgagcaaccc tgagacaaat   2220
68 acctcctcac agagcaacac ctcacaagaa gaagctgagg cgtcgcagtc agtactgtta   2280
69 cataaaagtc tcacttctga atgccacctt cttgaaccac caggcctcag ctgcaccagc   2340
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83 Glu Asn Arg His Arg Val Tyr Glu Arg Asn Arg His Phe Gly Leu Lys
84          35                  40                  45
85 Asp Val Asn Ile Pro Leu Glu Gly Arg Glu Leu Gly Asn Ile His Glu
86      50                  55                  60
87 Thr Ser Gln Asp Leu Ser Pro Glu Lys Ala Ser Ser Lys Thr Arg Ser
88 65                  70                  75                  80
89 Val Lys Met Val Leu Ser Asp Gln Arg Lys Gln Leu Leu Gln Lys Tyr
90              85                  90                  95
91 Lys Glu Glu Lys Gln Leu Gln Lys Leu Lys Glu Gln Arg Glu Lys Ala
92              100                 105                 110
93 Lys Arg Gly Val Phe Lys Val Gly Leu Tyr Arg Pro Ala Ala Pro Gly
94          115                 120                 125
95 Phe Leu Val Thr Asp Gln Arg Gly Ala Lys Ala Glu Pro Glu Lys Ala
96      130                 135                 140
97 Phe Pro His Thr Gly Arg Ile Thr Arg Ser Lys Thr Lys Glu Tyr Met
98 145                 150                 155                 160
99 Glu Gln Thr Lys Ile Gly Ser Arg Asn Val Pro Lys Ala Thr Gln Ser
100             165                 170                 175
101 Asp Gln Arg Gln Thr Ser Glu Lys Gln Pro Leu Asp Arg Glu Arg Lys
102             180                 185                 190
103 Val Met Gln Pro Val Leu Phe Thr Ser Gly Lys Gly Thr Glu Ser Ala
104         195                 200                 205
105 Ala Thr Gln Arg Ala Lys Leu Met Ala Arg Thr Val Ser Ser Thr Thr
106     210                 215                 220
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108 225             230             235                 240
109 Arg Pro Ser Gly Gly Arg Pro Ala Lys Lys Pro Glu Gly Lys Pro Asp
110             245             250                 255
111 Lys Val Ile Pro Ser Lys Val Glu Arg Asp Glu Lys His Leu Asp Ser
112             260             265                 270
113 Gln Thr Arg Glu Thr Ser Glu Met Gly Leu Leu Gly Val Phe Arg Glu
114         275             280                 285
115 Val Glu Ser Leu Pro Ala Thr Ala Pro Ala Gln Gly Lys Glu Arg Lys
116     290             295                 300
117 Ser Phe Ala Pro Lys His Cys Val Phe Gln Pro Pro Cys Gly Leu Lys
118 305             310             315                 320
119 Ser Tyr Gln Val Ala Pro Leu Ser Pro Arg Ser Ala Asn Ala Phe Leu
120             325             330                 335
121 Thr Pro Asn Cys Asp Trp Asn Gln Leu Arg Pro Glu Val Phe Ser Thr
122             340             345                 350
123 Thr Thr Gln Asp Lys Ala Asn Glu Ile Leu Val Gln Gln Gly Leu Glu
124         355             360                 365
125 Ser Leu Thr Asp Arg Ser Lys Glu His Val Leu Asn Gln Lys Gly Ala
126     370             375             380
127 Ser Thr Ser Asp Ser Asn His Ala Ser Val Lys Gly Val Pro Cys Ser
128 385             390             395                 400
129 Glu Gly Ser Glu Gly Gln Thr Ser Gln Pro Pro His Asp Val Pro Tyr
130             405             410                 415
131 Phe Arg Lys Ile Leu Gln Ser Glu Thr Asp Arg Leu Thr Ser His Cys
132             420             425                 430
133 Leu Glu Trp Glu Gly Lys Leu Asp Leu Asp Ile Ser Asp Glu Ala Lys
134         435             440                 445
135 Gly Leu Ile Arg Thr Thr Val Gly Gln Thr Arg Leu Leu Ile Lys Glu
136     450             455                 460
137 Arg Phe Arg Gln Phe Glu Gly Leu Val Asp Asn Cys Glu Tyr Lys Arg
138 465             470             475                 480
139 Gly Glu Lys Glu Thr Thr Cys Thr Asp Leu Asp Gly Phe Trp Asp Met
140             485             490                 495
141 Val Ser Phe Gln Val Asp Asp Val Asn Gln Lys Phe Asn Asn Leu Ile
142             500             505                 510
143 Lys Leu Glu Ala Ser Gly Trp Lys Asp Ser Asn Asn Pro Ser Lys Lys
144         515             520                 525
145 Val Leu Arg Lys Lys Ile Val Pro Gly Arg Thr Ser Lys Ala Lys Gln
146     530             535                 540
147 Asp Asp Asp Gly Arg Ala Ala Ala Arg Ser Arg Leu Ala Ala Ile Lys
148 545             550             555                 560
149 Asn Ala Met Lys Gly Arg Pro Gln Gln Glu Val Gln Ala His Ala Ala
150             565             570                 575
151 Ala Pro Glu Thr Thr Lys Glu Val Asp Lys Ile Val Phe Asp Ala Gly
152             580             585                 590
153 Phe Phe Arg Ile Glu Ser Pro Val Lys Ser Phe Ser Val Leu Ser Ser
154         595             600                 605
155 Glu Arg Arg Ser Gln Arg Phe Gly Thr Pro Leu Ser Ala Ser Lys Val
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156      610              .  615                 620
157 Val Pro Glu Gly Arg Ala Ala Gly Asp Leu Leu Arg Gln Lys Met Pro
158 625                  630              635                 640
159 Leu Lys Lys Pro Asp Pro Gln Ser Ser Lys Ser Glu His Val Asp Arg
160                  645              650                 655
161 Thr Phe Ser Asp Gly Leu Glu Ser Arg Cys His Val Glu Asp Thr Pro
162                  660              665                 670
163 Cys Pro Gly Glu Gln Asp Ser Ser Asp Ile Glu His Asp Val Asn Lys
164          675              680                 685
165 Ile Asn Val Lys Met Asp Cys Phe Ser Val Glu Thr Asn Leu Pro Leu
166      690              695                 700
167 Pro Ala Gly Asp Ala Asn Thr Asn Gln Lys Glu Ala Ile Ser Ala Val
168 705                  710              715                 720
169 Glu Gly Ala Ser Thr Ala Val Thr Ser Gln Asp Leu Leu Met Ser Asn
170                  725              730                 735
171 Pro Glu Thr Asn Thr Ser Ser Gln Ser Asn Thr Ser Gln Glu Glu Ala
172                  740              745                 750
173 Glu Ala Ser Gln Ser Val Leu Leu His Lys Ser Leu Thr Ser Glu Cys
174          755              760                 765
175 His Leu Leu Glu Pro Pro Gly Leu Ser Cys Thr Ser Pro Cys Thr Arg
176      770              775                 780
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183 <211> LENGTH: 2538
184 <212> TYPE: DNA
185 <213> ORGANISM: Homo sapiens
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190 cgaaatagac actttggttt gaaagatgta aacattccaa ccttggaagg tagaattctt     180
191 gttgaattag atgagacatc tcaagagctt gttccagaaa agaccaatgt taagccaagg     240
192 gcaatgaaaa ctattctagg tgatcaacga aaacagatgc tccaaaaata caaagaagaa     300
193 aagcaacttc aaaaattgaa agagcagaga gagaaagcta aacgaggaat atttaaagtg     360
194 ggtcgttata gacctgatat gccttgtttt cttttatcaa accagaatgc tgtgaaagct     420
195 gagccaaaaa aggctattcc atcttctgta cggattacaa ggtcaaaggc caaagaccaa     480
196 atggagcaga ctaagattga taacgagagt gatgttcgag caatccgacc tggtccaaga     540
197 caaacttctg aaaagaaagt gtcagacaaa gagaaaaaag ttgtgcagcc tgtaatgccc     600
198 acgtcgttga gaatgactcg atcagctact caagcagcaa agcaggttcc cagaacagtc     660
199 tcatctacca cagcaagaaa gccagtcaca agagctgcta atgaaaacga accagaagga     720
200 aaggtgccaa gtaaaggaag acctgccaaa aatgtagaaa caaaacccga caagggtatt     780
201 tcttgtaaag tcgatagtga agaaaatact ttgaattcac aaactaatgc aacaagtgga     840
202 atgaatccag atggagtctt atcaaaaatg gaaaacttac ctgagataaa tactgcaaaa     900
203 ataaaaggga agaattcctt cgcacctaag gattttatgt ttcagccact ggatggtctg     960
204 aagacctatc aagtaacacc tatgactccc agaagtgcca atgctttttt gacacccagt    1020
205 tacacctgga ctcctttaaa aacagaagtt gatgagtctc aagcaacaaa agaaattttg    1080
206 gcacaaaaat gtaaaactta ctctaccaag acaatacagc aagattcaaa taaattgcca    1140
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209 ggtcgaattg ctcagcccca ccatggtgtg ccatatttca gaaatatcct ccagtcagaa   1320
210 actgagaaat taacttcaca ttgcttcgag tgggacagga aacttgaatt ggacattcca   1380
211 gatgatgcta aagatcttat tcgcacagca gttggtcaaa caagactcct tatgaaggaa   1440
212 aggtttaaac agtttgaagg actggttgat gattgtgaat ataaacgagg tataaaggag   1500
213 actacctgta cagatctgga tggattttgg gatatggtta gttttcagat agaagatgta   1560
214 atccacaaat tcaacaatct gatcaaactt gaggaatctg ggtggcaagt caataataat   1620
215 atgaatcata atatgaacaa aaatgtcttt aggaaaaaag ttgtctcagg tatagcaagt   1680
216 aaaccaaaac aggatgatgc tggaagaatt gcagcgagaa atcgcctagc tgccataaaa   1740
217 aatgcaatga gagagagaat taggcaggaa gaatgtgctg aaacagcagt ttctgtgata   1800
218 ccaaaggaag ttgataaaat agtgttcgat gctggatttt tcagagttga aagtcctgtt   1860
219 aaattattct caggactttc tgtctcttct gaaggccctt ctcaaagact tggaacacct   1920
220 aagtctgtca acaaagctgt atctcagagt agaaatgaga tgggcattcc acaacaaact   1980
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222 tttttgagta ttcctgaaag caggagcagc atagaagatg ctcagtgtcc tggattacca   2100
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227 gaaggggaaa ctaaaatttc tcagtcagaa ctatttgata ataaaagtct cactactgaa   2400
228 tgccaccttc ttgattcacc aggtctaaac tgcagtaatc catttactca gctggagagg   2460
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233 <211> LENGTH: 846
234 <212> TYPE: PRT
235 <213> ORGANISM: Homo sapiens
237 <400> SEQUENCE: 4

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241             20                  25                  30
242 Glu Asn Arg His Lys Glu Tyr Glu Arg Asn Arg His Phe Gly Leu Lys
243         35                  40                  45
244 Asp Val Asn Ile Pro Thr Leu Glu Gly Arg Ile Leu Val Glu Leu Asp
245     50                  55                  60
246 Glu Thr Ser Gln Glu Leu Val Pro Glu Lys Thr Asn Val Lys Pro Arg
247 65                  70                  75                  80
248 Ala Met Lys Thr Ile Leu Gly Asp Gln Arg Lys Gln Met Leu Gln Lys
249             85                  90                  95
250 Tyr Lys Glu Glu Lys Gln Leu Gln Lys Leu Lys Glu Gln Arg Glu Lys
251             100                 105                 110
252 Ala Lys Arg Gly Ile Phe Lys Val Gly Arg Tyr Arg Pro Asp Met Pro
253         115                 120                 125
254 Cys Phe Leu Leu Ser Asn Gln Asn Ala Val Lys Ala Glu Pro Lys Lys
255     130                 135                 140
256 Ala Ile Pro Ser Ser Val Arg Ile Thr Arg Ser Lys Ala Lys Asp Gln
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VERIFICATION SUMMARY
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